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**RAW SEQUENCE LISTING**  
PATENT APPLICATION: US/10/053,406

DATE: 02/06/2002  
TIME: 09:33:41

Input Set : N:\Crf3\RULE60\10053406.raw  
Output Set: N:\CRF3\02062002\J053406.raw

1 <110> APPLICANT: Debinski, Waldemar  
2           Thompson, Jeffrey  
3 <120> TITLE OF INVENTION: IL13 MUTANTS  
4 <130> FILE REFERENCE: 6460-28  
5 <140> CURRENT APPLICATION NUMBER: 10/053,406  
6 <141> CURRENT FILING DATE: 2002-01-17  
8 <150> PRIOR APPLICATION NUMBER: US/09/679,710B  
9 <151> PRIOR FILING DATE: 2001-06-04  
12 <160> NUMBER OF SEQ ID NOS: 23  
13 <170> SOFTWARE: PatentIn version 3.0  
15 <210> SEQ ID NO: 1  
16 <211> LENGTH: 114  
17 <212> TYPE: PRT  
18 <213> ORGANISM: Homo sapiens  
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21            1               5               10               15  
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23            20              25               30  
24       Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala  
25            35              40               45  
26       Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr  
27            50              55               60  
28       Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln  
29            65              70               75               80  
30       Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe  
31            85              90               95  
32       Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg  
33            100             105              110  
34       Phe Asn  
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42 <223> OTHER INFORMATION: hIL13 mutant having a Glu to Lys substitution at  
43 residue 13  
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45       Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Lys Leu Ile Glu  
46            1               5               10               15  
47       Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly  
48            20              25               30

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49       Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala  
50                 35                 40                 45  
51       Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr  
52                 50                 55                 60  
53       Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln  
54                 65                 70                 75                 80  
55       Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe  
56                 85                 90                 95  
57       Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg  
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65 <220> FEATURE:  
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67 <223> OTHER INFORMATION: hIL13 mutant having a Glu to Ile substitution at  
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70       Ser Pro Gly Pro Val Pro Ser Thr Ala Leu Arg Ile Leu Ile Glu  
71                 1                 5                 10                 15  
72       Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly  
73                 20                 25                 30  
74       Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala  
75                 35                 40                 45  
76       Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr  
77                 50                 55                 60  
78       Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln  
79                 65                 70                 75                 80  
80       Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe  
81                 85                 90                 95  
82       Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg  
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84       Phe Asn  
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89 <213> ORGANISM: ARTIFICIAL SEQUENCE  
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91 <221> NAME/KEY: misc\_feature  
92 <223> OTHER INFORMATION: hIL13 mutant having a Glu to Cys substitution at  
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97       Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly  
98                 20                 25                 30  
99       Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala

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100               35                          40                          45  
 101   Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr  
 102       50                               55                           60  
 103   Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln  
 104       65                               70                           75                           80  
 105   Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe  
 106       85                               90                           95  
 107   Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg  
 108       100                              105                           110  
 109   Phe Asn  
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 116 <221> NAME/KEY: misc\_feature  
 117 <223> OTHER INFORMATION: hIL13 mutant having a Glu to Ser substitution at  
 118 residue 13  
 119 <400> SEQUENCE: 5  
 120   Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Ser Leu Ile Glu  
 121       1                               5                           10                           15  
 122   Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly  
 123       20                              25                           30  
 124   Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala  
 125       35                              40                           45  
 126   Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr  
 127       50                              55                           60  
 128   Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln  
 129       65                              70                           75                           80  
 130   Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe  
 131       85                              90                           95  
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 134   Phe Asn  
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 142 <223> OTHER INFORMATION: hIL13 mutant having a Glu to Arg substitution at  
 143 residue 13  
 144 <400> SEQUENCE: 6  
 145   Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Arg Leu Ile Glu  
 146       1                              5                           10                           15  
 147   Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly  
 148       20                              25                           30  
 149   Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala  
 150       35                              40                           45

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151 Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr  
152 50 55 60  
153 Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln  
154 65 70 75 80  
155 Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe  
156 85 90 95  
157 Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg  
158 100 105 110  
159 Phe Asn  
161 <210> SEQ ID NO: 7  
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163 <212> TYPE: PRT  
164 <213> ORGANISM: ARTIFICIAL SEQUENCE  
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166 <221> NAME/KEY: misc\_feature  
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168 residue 13  
169 <400> SEQUENCE: 7  
170 Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Tyr Leu Ile Glu  
171 1 5 10 15  
172 Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly  
173 20 25 30  
174 Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala  
175 35 40 45  
176 Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr  
177 50 55 60  
178 Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln  
179 65 70 75 80  
180 Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe  
181 85 90 95  
182 Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg  
183 100 105 110  
184 Phe Asn  
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192 <223> OTHER INFORMATION: hIL13 mutant having a Glu to Asp substitution at  
193 residue 13  
194 <400> SEQUENCE: 8  
195 Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Asp Leu Ile Glu  
196 1 5 10 15  
197 Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly  
198 20 25 30  
199 Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala  
200 35 40 45  
201 Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr

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202               50               55               60  
203 Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln  
204         65               70               75               80  
205 Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe  
206               85               90               95  
207 Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg  
208               100              105              110  
209 Phe Asn  
211 <210> SEQ ID NO: 9  
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214 <213> ORGANISM: ARTIFICIAL SEQUENCE  
215 <220> FEATURE:  
216 <221> NAME/KEY: misc\_feature  
217 <223> OTHER INFORMATION: hIL13 mutant having a Glu to Lys substitution at  
218 residue 16  
219 <400> SEQUENCE: 9  
220 Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Glu Leu Ile Lys  
221         1               5               10               15  
222 Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly  
223         20               25               30  
224 Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala  
225         35               40               45  
226 Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr  
227         50               55               60  
228 Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln  
229         65               70               75               80  
230 Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe  
231         85               90               95  
232 Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg  
233         100              105              110  
234 Phe Asn  
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242 <223> OTHER INFORMATION: hIL13 mutant having a Glu to Lys substitution at  
243 residue 17  
244 <400> SEQUENCE: 10  
245 Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Glu Leu Ile Glu  
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247 Lys Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly  
248         20               25               30  
249 Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala  
250         35               40               45  
251 Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr  
252         50               55               60

**VERIFICATION SUMMARY**

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